```
        9       18       27       36       45       54
NGG GGG GCG  TAC GGA GGT  GGC AGC TGT  GGG AGG AGG  CGG CGT GGA  AGG CCG AGG

       63       72       81       90       99      108
AGC TCA AGC  CCG GAC CAA  TCC CCA CCC  CGT TCC GGG  CCC TGC TGA  CCC TGC AGC

      117      126      135      144      153      162
GTA CCG GGA  AGC GAA ACC  GGC CGG ATG  GGC CGC ATC  GGC CGA GCC  CAC CAC TGT

      171      180      189      198      207      216
GTG GAG CCT  GGA GCT GAG  ATC AGG ATG  TTC CGC TTC  ATG AGG GAC  GTG GAG
                               M    F    R    F    M    R    D    V    E

      225      234      243      252      261      270
CCT GAG GAT  CCC ATG TTC  CTG CCC TTT  GCT ATT CAC  CGT CAG CAT  ATG
 P   E   D    P   M   F    L   P   F    A   I   H    R   Q   H    M

      279      288      297      306      315      324
AGC CGT ATG  TTG TCA GGT  TTT GGA TAT  AGC CCC TTC  CTC AGC ATC  ACA GAT
 S   R   M    L   S   G    F   G   Y    S   P   F    L   S   I    T   D

      333      342      351      360      369      378
GGC AAC CCA  GGG ACC AGG  GCT GCC AGC  CGC ATG CAG  CAG GCT GGA  GCT
 G   N   P    G   T   R    A   A   S    R   M   Q    Q   A   G    A

      387      396      405      414      423      432
GTC TNC TTT  GGG NTG CTG  GGA ATG TCG  GGT GGT TTC  ATG GAC ATG  TTT GGG
 V   P   F    G   X   L    G   M   S    G   G   F    M   D   M    F   G
```

FIGURE 1A

```
        441                     450                     459                     468                     477                     486
        ATG ATG GAC     ATG NTT GGA     AAC ATG GAA     CAC ATG ACA     GCT GGA GGC     AAT TGC
         M   M   D       M   X   G       N   M   E       H   M   T       A   G   G       N   C

        495                     504                     513                     522                     531                     540
        CAG ACC TTC     TCA TCT TCC     ACT GTC TCC     TAC ATC AAT     ACG GGT GAT     GGT GCC
         Q   T   F       S   S   S       T   V   S       Y   I   N       T   G   D       G   A

        549                     558                     567                     576                     585                     594
        CCC AAG GTC     TAC CAA GAG     ACA TCA ATG     CGC TCG GCA     CCA GGC GGG     ATC CGG
         P   K   V       Y   Q   E       T   S   M       R   S   A       P   G   G       I   R

        603                     612                     621                     630                     639                     648
        GAG ACA CGG     AGG ACT GTT     CGG GAT TCA     GAC AGT GAG     CTG GAG CAG     ATG TCC ATT
         E   T   R       R   T   V       R   D   S       D   S   E       L   E   Q       M   S   I

        657                     666                     675                     684                     693                     702
        GGG CAT CAC     ATC CGG GAC     AGG GCT CAC     ATC CTC CAG     CGC TCC AAC     CAT CGC
         G   H   H       I   R   D       R   A   H       I   L   Q       R   S   N       H   R

        711                     720                     729                     738                     747                     756
        GGG GAC CAG     GAG CGG CAG     GAC TAT ATC     AAC CTG GAT     GAG AGT GAG     GCC
         G   D   Q       E   R   Q       D   Y   I       N   L   D       E   S   E       A

        765                     774                     783                     792                     801                     810
        GCA GCG TTT     GAT GAC TGG     CGG GAG ACC     TCC CGA TTC     CGG CAG CAG     CGT
         A   A   F       D   D   W       R   E   T       S   R   F       R   Q   Q       R
```

FIGURE 1B

```
                    819                 828                 837                 846                 855                 864
                    CCC   CTG   GAG     TTT   CGG   CTT     GAG   TCA   GGG     GCT   GGG   GGA     CGA   AGG   GCG     GAG
                    P     L     E       F     R     L       E     S     G       A     G     R       R     A             E

                    873                 882                 891                 900                 909                 918
                    GGG   CCT   CCC     CGC   CTG   GCC     ATC   CAG   GGA     CCT   GAG   GAC     TCC   CTT   CCC     GAC   AGT   CCC
                    G     P     P       R     L     A       I     Q     G       P     E     D       S     L     P       D     S     P

                    927                 936                 945                 954                 963                 972
                    GCC   GCT   ATG     ACT   GGT   GAG     GGC   CCC   GGG     GCC   TCA   GCT     CTC   TTG   TAC     AGG   CTG   AGA
                    A     A     M       T     G     E       G     P     G       A     S     A       L     L     Y       R     L     R

                    981                 990                 999                 1008                1017                1026
                    GGC   TGA   ATC     ATC   CCC   TGA     ATA   ACT   TTT     TCC   TCT   CGA     TTC   CCA   TCC     CCA   ATT
                    G     *     E       I     I     P       *     I     T       F     S     S       R     F     P       S     P     I

                    1035                1044                1053                1062                1071                1080
                    TAA   TAT   TAA     ATT   AAC   AGG     CAA   GCC   GGC     CCC   CAC   CTC     TCC   CTG   GGG     GTC   TCA   GGG
                    *     Y     *       I     N     R       Q     A     G       P     H     L       S     L     G       V     S     G

                    1089                1098                1107                1116                1125                1134
                    AGA   ACC   TTT     CAC   GGC   ACC     CTT   TCC   CTA     CCT   TTT   CCT     TTA   ATC   TCC     TGG   TTT
                    R     T     F       H     G     T       L     S     L       P     F     P       L     I     S       W     F

                    1143                1152                1161                1170                1179                1188
                    ACC   ATT   GAT     GAC   TTC   GGC     TCT   GCA   TCT     ACT   TAC   TTG     ATT   TTT   CAT     TCT   GCC   ACT
                    T     I     D       D     F     G       S     A     S       T     Y     L       I     F     H       S     A     T
```

FIGURE 1C

```
                1206      1215      1224      1233      1242
      1197
TCA TCT TCA AAC CCC CTC ACC TTT CCC ATC CTA CTC CTG CCA TGC ATT GAA GGG
 S   S   S   N   P   L   T   F   P   I   L   L   L   P   C   I   E   G

                1260      1269      1278      1287      1296
      1251
TCA ATG CAT TTT GGG GTG AGN TTN GGT TTA GGG GCC CCT TCA TNC CTN AGC TAC
 S   M   H   F   G   V   X   X   G   L   G   A   P   S   X   L   S   Y

                1314      1323
      1305
CTG GGT TGC CTT CCA ACT TTT CTC AGA
 L   G   C   L   P   T   F   L   R
```

FIGURE 1D

```
  1   MFRFMRDVEPEDPMFLMDPFFAIHRQHMSRM    762280
  1   MFRMLNSSFEDDP-FFSESILAHRENMRQM     GI 1066392
  1   MFRFMRDVEPEDPMFLMDPFFAIHRQHMSRM    GI 1399745

 31   L--SGGFGYSPFLSITDGNMPGTRAASRR       762280
 30   IRSFSEPFG-RDLLSISDGR--GRAHNRR       GI 1066392
 31   L--SGGFGYSPFLSITDGNMPGTRPASRR       GI 1399745

 58   MQQAGA----VXPFGXLGMSGGFMDMF         762280
 56   GHNDGEDSLTHTDVSSFQTMDQMVSNMRNY      GI 1066392
 58   MQQAGA---VSPFGMLGMSGGFMDMF          GI 1399745

 81   GMMNDMXGNMEHMTAGGNCQTFSSSTVISY      762280
 86   -MQKLERNFGQLSVDPNGHSFCSSSVMTY       GI 1066392
 81   GMMNDMIGNMEHMTAGGNCQTFSSSTVISY      GI 1399745

111   SNTGDGAPKVYQETSEMRSAPGGIRETRRT      762280
114   SKIGDEPPKVFQASTQTRRAPGGIKETRKA      GI 1066392
111   SNTGDGAPKVYQETSEMRSAPGGIRETRRT      GI 1399745

141   VRDSDSGLEQMSIGHHIRDRAHILQRSRNH      762280
144   MRDSDSGLEKMAIGHHIHDRAHVIKKSKNK      GI 1066392
141   VRDSDSGLEQMSIGHHIRDRAHILQRSRNH      GI 1399745
```

FIGURE 2A

```
171  R T G D Q E E R Q D Y I N L D E S E A A A F D D E W R R E T      762280
174  K T G D E E V N Q E F I N M N E S D A H A F D D E E W Q S E V     GI 1066392
171  R T G D Q E E R Q D Y I N L D E S E A A A F D D D E W R R E T     GI 1399745

201  S R F R Q Q R P - L E F R R L E S S G A G - - G R R A E G P       762280
204  L K Y K P G R H N L G N T R M R S V G H E N P G S R E L K R       GI 1066392
201  S R F R Q Q R P - L E F R R L E S S G A G - - G R R A E G P       GI 1399745

228  P R L A I Q G P E D S L P D S P A A M T G E G P G A S A L L       762280
234  R E K P Q Q S P A I E H G R R S N V L G D K L H I K G S S V       GI 1066392
228  P R L A I Q G P E D S - - - - - - - - - - - - P S R Q S R R .     GI 1399745

258  Y R L R G                                                        762280
264  K S N K K                                                        GI 1066392
246  Y D W                                                            GI 1399745
```
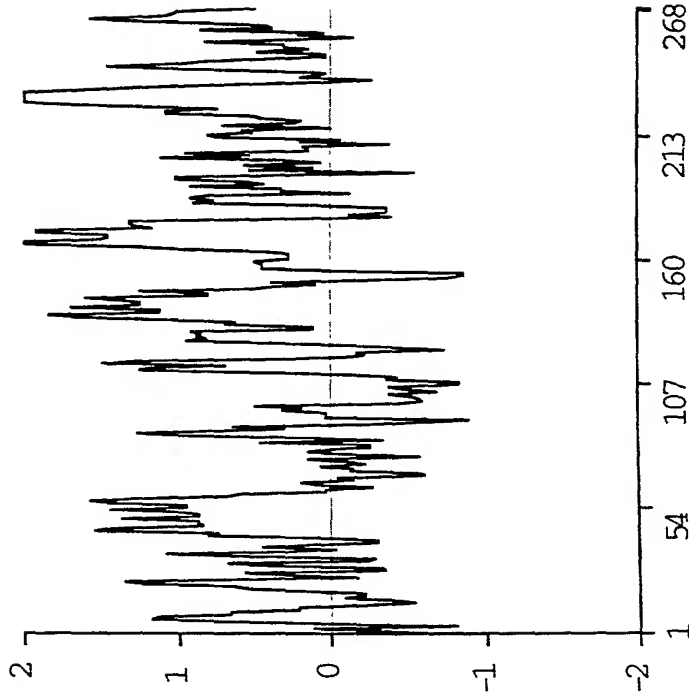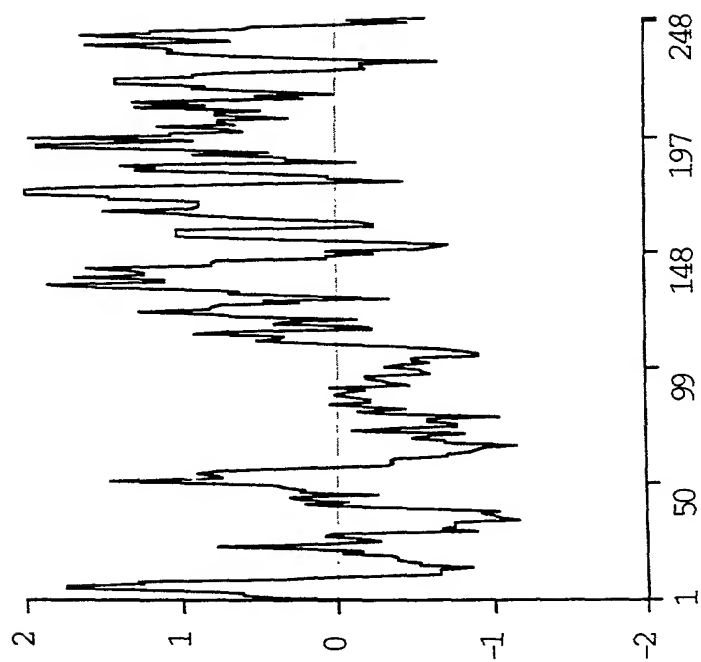
FIGURE 2B
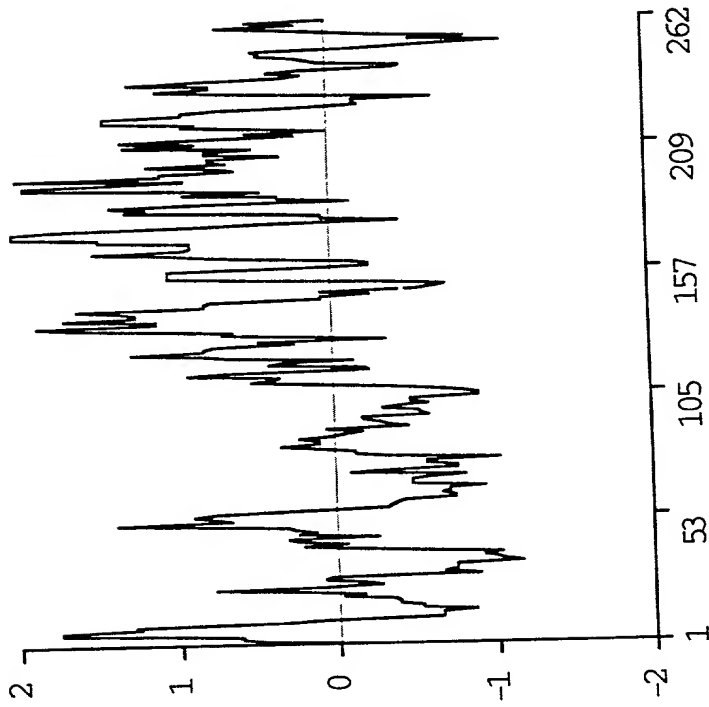
FIGURE 3A

FIGURE 3B

FIGURE 3C

Library	Lib Description	Abun	Pct Abun
BRAINOT11	brain, right temporal, epilepsy, 5 M	4	0.1289
PITUNOT03	pituitary, 46 M	3	0.1045
BRAINOM02	brain, 55 M, NORM, WM	2	0.0907
PGANNOT03	paraganglionic tumor, 46 M	2	0.0622
STOMNOT02	stomach, 52 M, match to STOMTUT01	2	0.0615
BRAINOT12	brain, right frontal, epilepsy, 5 M	2	0.0607
PROSNOT05	prostate, 67 M, match to PROSTUT03	1	0.0576
HNT3AZT01	hNT2 cell line, treated AZ	3	0.0572
BMARNOT03	bone marrow, 16 M	2	0.0484
BRSTNOT03	breast, 54 F, match to BRSTTUT	3	0.0441
STOMTUT01	stomach tumor, 52 M,	1	0.0368
BRAINOT04	brain, choroid plexus, 44 M	1	0.0356
BRAINOT10	brain, cerebellum, Alzheimer's, 74 M	1	0.0348
HNT2NOT01	hNT2 cell line, control	2	0.0345
MMLR3DT01	macrophages (adher PBMNC), 72-hr MLR	1	0.0332
SPLNFEM01	spleen, fetal, WM	1	0.0332
BRAINOT14	brain, 40 F, match BRAITUT12	1	0.0315
NEUTGMT01	granulocytes, M/F, treated GM-CSF	2	0.0313
THYRNOT02	thyroid, hyperthyroidism, 16 F	1	0.0303
BRAINON01	brain, 26 M, NORM	3	0.0296
TONGTUT01	tongue tumor, carcinoma, 36 M	1	0.0295
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293
BEPINOT01	bronchial epithelium, 54 M	2	0.0289
FIBRSEM01	fibroblasts, senescent, NORM, WM	1	0.0289
COLNNOT05	colon, 40 M, match to COLNCRT01	1	0.0289
STOMTUT02	stomach tumor, lymphoma, 68 F	1	0.0284
PROSNOT11	prostate, 28 M	1	0.0282
BRSTTUT02	breast tumor, 54 F, match BRSTNOT03	2	0.0279
BLADNOT04	bladder and seminal vesicle, 28 M	1	0.0278
UTRSNOT05	uterus, 45 F	1	0.0278
PROSNOT19	prostate, 59 M	1	0.0272
BRAINOM03	brain, 55 M, NORM, WM	1	0.0270
ENDCNOT01	endothelial cells, coronary artery, 58 M	1	0.0268
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267
PENITUT01	penis tumor, carcinoma, 64 M	1	0.0267
LNODNOT03	lymph node, 67 M	1	0.0265
LEUKNOT03	white blood cells, 27 F	1	0.0262
URETTUT01	ureter tumor, 69 M	1	0.0262
ENDANOT01	endothelial cells, aorta, M	2	0.0257
PROSNOT18	prostate, 58 M	1	0.0256
BRSTTUT08	breast tumor, 45 F, match to BRSTNOT09	1	0.0254
SPLNFET02	spleen, fetal M	2	0.0252
UTRSNOT02	uterus, 34 F	3	0.0233
PROSNOT06	prostate, 57 M, match to PROSTUT04	2	0.0229
NERVMSM01	multiple sclerosis, 46 M, NORM, WM	1	0.0224
ENDCNOT03	endothelial cells, neonatal M	1	0.0210
OVARTUT01	ovarian tumor, 43 F	2	0.0207
UTRPNOM01	uterus, F, NORM, WM	1	0.0201
LUNGNOT03	lung, 79 M, match to LUNGTUT02	1	0.0200

FIGURE 4A

BRSTNOT04	breast, 62 F	2	0.0192
BRSTTUT01	breast tumor, 55 F, match BRSTNOT02	2	0.0189
HNT2RAT01	hNT2 cell line, treated RA	1	0.0188
BRAINOT09	brain, fetal M	2	0.0186
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	1	0.0180
MMLR2DT01	macrophages (adher PBMNC), 48-hr MLR	1	0.0178
SINTBST01	small intestine, ileum, Crohn's, 18 F	1	0.0168
PGANNOT01	paraganglionic tumor, 46 M	1	0.0160
BRSTNOT05	breast, 58 F, match to BRSTTUT03	2	0.0149
CONNNOT01	fat, mesentery, 71 M	1	0.0149
BRSTNOT07	breast, 43 F	1	0.0146
NGANNOT01	ganglioneuroma, 9 M	2	0.0146
COLNFET02	colon, fetal F	1	0.0143
LUNGFET03	lung, fetal F	2	0.0138
THYRNOT03	thyroid tumor, adenoma, 28 F	1	0.0138
LATRTUT02	heart tumor, myoma, 43 M	1	0.0137
PITUNOT02	pituitary, 15-75 M/F	1	0.0135
BRAINOM01	brain, infant F, NORM, WM	3	0.0134
PROSNOT16	prostate, 68 M	1	0.0132
CONUTUT01	mesentery tumor, sigmoid, 61 F	1	0.0130
BLADTUT04	bladder tumor, 60 M, match BLADNOT05	1	0.0127
PROSTUT04	prostate tumor, 57 M, match PROSNOT06	1	0.0117
KIDNNOT05	kidney, neonatal F	1	0.0106
MELANOM01	melanocytes, M, NORM, WM	1	0.0096
PROSNON01	prostate, 28 M, NORM	1	0.0094
BRAITUT02	brain tumor, metastasis, 58 M	1	0.0075
ISLTNOT01	pancreas, islet cells, M/F	1	0.0064
LIVSFEM02	liver/spleen, fetal M, NORM, WM	2	0.0053

FIGURE 4B